

# SEQUENCE LISTING

<110> Coleman, Timothy A. et al.

<120> Human Glycosylation Enzymes

<130> PF505D1

<150> PCT/US00/05325

<151> 2000-03-01

<150> 09/516,143

<151> 2000-03-01

<150> 60/122,409

<151> 1999-03-02

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 1305

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1302)

<220>

<221> SITE

<222> (397)..(399)

<223> yat encodes Tyr or His

<220>

<221> SITE

<222> (406)..(408)

<223> gkt encodes Gly or Val

<220>

<221> SITE

<222> (439)..(441)

<223> yca encodes Ser or Pro

<220>

<221> SITE

<222> (505)..(507)

<223> gkt encodes Gly or Val

<400> 1

atg	gac	tgc	gtg	gag	aag	ggg	gcc	gcc	acc	tcc	gtc	tcc	aac	ccg	cgg	48
Met	Asp	Ser	Val	Glu	Lys	Gly	Ala	Ala	Thr	Ser	Val	Ser	Asn	Pro	Arg	
1				5					10					15		

ggg	cga	ccg	tcc	cgg	ggc	cgg	ccg	ccg	aag	ctg	cag	cgc	aac	tct	cgc	96
Gly	Arg	Pro	Ser	Arg	Gly	Arg	Pro	Pro	Lys	Leu	Gln	Arg	Asn	Ser	Arg	
			20					25					30			

ggc	ggc	cag	ggc	cga	ggt	gtg	gag	aag	ccc	ccg	cac	ctg	gca	gcc	cta	144
Gly	Gly	Gln	Gly	Arg	Gly	Val	Glu	Lys	Pro	Pro	His	Leu	Ala	Ala	Leu	

35					40					45						
att	ctg	gcc	cgg	gga	ggc	agc	aaa	ggc	atc	ccc	ctg	aag	aac	att	aag	192
Ile	Leu	Ala	Arg	Gly	Gly	Ser	Lys	Gly	Ile	Pro	Leu	Lys	Asn	Ile	Lys	
50						55				60						
cac	ctg	gcg	ggg	gtc	ccg	ctc	att	ggc	tgg	gtc	ctg	cgt	gcg	gcc	ctg	240
His	Leu	Ala	Gly	Val	Pro	Leu	Ile	Gly	Trp	Val	Leu	Arg	Ala	Ala	Leu	
65				70						75				80		
gat	tca	ggg	gcc	ttc	cag	agt	gta	tgg	ggt	tcg	aca	gac	cat	gat	gaa	288
Asp	Ser	Gly	Ala	Phe	Gln	Ser	Val	Trp	Val	Ser	Thr	Asp	His	Asp	Glu	
				85				90						95		
att	gag	aat	gtg	gcc	aaa	caa	ttt	ggt	gca	caa	ggt	cat	cga	aga	agt	336
Ile	Glu	Asn	Val	Ala	Lys	Gln	Phe	Gly	Ala	Gln	Val	His	Arg	Arg	Ser	
		100						105				110				
tct	gaa	ggt	tca	aaa	gac	agc	tct	acc	tca	cta	gat	gcc	atc	ata	gaa	384
Ser	Glu	Val	Ser	Lys	Asp	Ser	Ser	Thr	Ser	Leu	Asp	Ala	Ile	Ile	Glu	
115						120						125				
ttt	ctt	aat	tat	yat	aat	gag	gkt	gac	att	gta	gga	aat	att	caa	gct	432
Phe	Leu	Asn	Tyr	Xaa	Asn	Glu	Xaa	Asp	Ile	Val	Gly	Asn	Ile	Gln	Ala	
130						135				140						
act	tct	yca	tgt	tta	cat	cct	act	gat	ctt	caa	aaa	ggt	gca	gaa	atg	480
Thr	Ser	Xaa	Cys	Leu	His	Pro	Thr	Asp	Leu	Gln	Lys	Val	Ala	Glu	Met	
145				150						155				160		
att	cga	gaa	gaa	gga	tat	gat	tct	gkt	ttc	tct	ggt	gtg	aga	cgc	cat	528
Ile	Arg	Glu	Glu	Gly	Tyr	Asp	Ser	Xaa	Phe	Ser	Val	Val	Arg	Arg	His	
				165				170						175		
cag	ttt	cga	tgg	agt	gaa	att	cag	aaa	gga	ggt	cgt	gaa	gtg	acc	gaa	576
Gln	Phe	Arg	Trp	Ser	Glu	Ile	Gln	Lys	Gly	Val	Arg	Glu	Val	Thr	Glu	
		180						185				190				
cct	ctg	aat	tta	aat	cca	gct	aaa	cgg	cct	cgt	cga	caa	gac	tgg	gat	624
Pro	Leu	Asn	Leu	Asn	Pro	Ala	Lys	Arg	Pro	Arg	Arg	Gln	Asp	Trp	Asp	
195						200						205				
gga	gaa	tta	tat	gaa	aat	ggc	tca	ttt	tat	ttt	gct	aaa	aga	cat	ttg	672
Gly	Glu	Leu	Tyr	Glu	Asn	Gly	Ser	Phe	Tyr	Phe	Ala	Lys	Arg	His	Leu	
210						215				220						
ata	gag	atg	ggg	tac	ttg	cag	ggg	gga	aaa	tgg	cat	act	acg	aaa	tgc	720
Ile	Glu	Met	Gly	Tyr	Leu	Gln	Gly	Gly	Lys	Trp	His	Thr	Thr	Lys	Cys	
225				230						235				240		
gag	ctg	gaa	cat	agt	gtg	gat	ata	gat	gtg	gat	att	gat	tgg	cct	att	768
Glu	Leu	Glu	His	Ser	Val	Asp	Ile	Asp	Val	Asp	Ile	Asp	Trp	Pro	Ile	
				245				250						255		
gca	gag	caa	aga	gta	tta	aga	tat	ggc	tat	ttt	ggc	aaa	gag	aag	ctt	816
Ala	Glu	Gln	Arg	Val	Leu	Arg	Tyr	Gly	Tyr	Phe	Gly	Lys	Glu	Lys	Leu	
		260				265						270				
aag	gaa	ata	aaa	ctt	ttg	ggt	tgc	aat	att	gat	gga	tgt	ctc	acc	aat	864
Lys	Glu	Ile	Lys	Leu	Leu	Val	Cys	Asn	Ile	Asp	Gly	Cys	Leu	Thr	Asn	
275						280						285				

ggc cac att tat gta tca gga gac caa aaa gaa ata ata tct tat gat	912
Gly His Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp	
290 295 300	
gta aaa gat gct att ggg ata agt tta tta aag aaa agt ggt att gag	960
Val Lys Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu	
305 310 315 320	
gtg agg cta atc tca gaa agg gcc tgt tca aag cag acg ctg tct tct	1008
Val Arg Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser	
325 330 335	
tta aaa ctg gat tgc aaa atg gaa gtc agt gta tca gac aag cta gca	1056
Leu Lys Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala	
340 345 350	
gtt gta gat gaa tgg aga aaa gaa atg ggc ctg tgc tgg aaa gaa gtg	1104
Val Val Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val	
355 360 365	
gca tat ctt gga aat gaa gtg tct gat gaa gag tgc ttg aag aga gtg	1152
Ala Tyr Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val	
370 375 380	
ggc cta agt ggc gct cct gct gat gcc tgt tcc tac gcc cag aag gct	1200
Gly Leu Ser Gly Ala Pro Ala Asp Ala Cys Ser Tyr Ala Gln Lys Ala	
385 390 395 400	
gtt gga tac att tgc aaa tgt aat ggt ggc cgt ggt gcc atc cga gaa	1248
Val Gly Tyr Ile Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu	
405 410 415	
ttt gca gag cac att tgc cta cta atg gaa aaa gtt aat aat tca tgc	1296
Phe Ala Glu His Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys	
420 425 430	
caa aaa tag	1305
Gln Lys	

<210> 2  
 <211> 434  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SITE  
 <222> 133  
 <223> Xaa equals Tyr or His

<220>  
 <221> SITE  
 <222> 136  
 <223> Xaa equals Gly or Val

<220>  
 <221> SITE  
 <222> 147  
 <223> Xaa equals Ser or Pro

<220>  
 <221> SITE  
 <222> 169  
 <223> Xaa equals Gly or Val

<400> 2

Met	Asp	Ser	Val	Glu	Lys	Gly	Ala	Ala	Thr	Ser	Val	Ser	Asn	Pro	Arg	1	5	10	15
Gly	Arg	Pro	Ser	Arg	Gly	Arg	Pro	Pro	Lys	Leu	Gln	Arg	Asn	Ser	Arg	20	25	30	
Gly	Gly	Gln	Gly	Arg	Gly	Val	Glu	Lys	Pro	Pro	His	Leu	Ala	Ala	Leu	35	40	45	
Ile	Leu	Ala	Arg	Gly	Gly	Ser	Lys	Gly	Ile	Pro	Leu	Lys	Asn	Ile	Lys	50	55	60	
His	Leu	Ala	Gly	Val	Pro	Leu	Ile	Gly	Trp	Val	Leu	Arg	Ala	Ala	Leu	65	70	75	80
Asp	Ser	Gly	Ala	Phe	Gln	Ser	Val	Trp	Val	Ser	Thr	Asp	His	Asp	Glu	85	90	95	
Ile	Glu	Asn	Val	Ala	Lys	Gln	Phe	Gly	Ala	Gln	Val	His	Arg	Arg	Ser	100	105	110	
Ser	Glu	Val	Ser	Lys	Asp	Ser	Ser	Thr	Ser	Leu	Asp	Ala	Ile	Ile	Glu	115	120	125	
Phe	Leu	Asn	Tyr	Xaa	Asn	Glu	Xaa	Asp	Ile	Val	Gly	Asn	Ile	Gln	Ala	130	135	140	
Thr	Ser	Xaa	Cys	Leu	His	Pro	Thr	Asp	Leu	Gln	Lys	Val	Ala	Glu	Met	145	150	155	160
Ile	Arg	Glu	Glu	Gly	Tyr	Asp	Ser	Xaa	Phe	Ser	Val	Val	Arg	Arg	His	165	170	175	
Gln	Phe	Arg	Trp	Ser	Glu	Ile	Gln	Lys	Gly	Val	Arg	Glu	Val	Thr	Glu	180	185	190	
Pro	Leu	Asn	Leu	Asn	Pro	Ala	Lys	Arg	Pro	Arg	Arg	Gln	Asp	Trp	Asp	195	200	205	
Gly	Glu	Leu	Tyr	Glu	Asn	Gly	Ser	Phe	Tyr	Phe	Ala	Lys	Arg	His	Leu	210	215	220	
Ile	Glu	Met	Gly	Tyr	Leu	Gln	Gly	Gly	Lys	Trp	His	Thr	Thr	Lys	Cys	225	230	235	240
Glu	Leu	Glu	His	Ser	Val	Asp	Ile	Asp	Val	Asp	Ile	Asp	Trp	Pro	Ile	245	250	255	
Ala	Glu	Gln	Arg	Val	Leu	Arg	Tyr	Gly	Tyr	Phe	Gly	Lys	Glu	Lys	Leu	260	265	270	
Lys	Glu	Ile	Lys	Leu	Leu	Val	Cys	Asn	Ile	Asp	Gly	Cys	Leu	Thr	Asn	275	280	285	

Gly His Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp  
 290 295 300  
 Val Lys Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu  
 305 310 315 320  
 Val Arg Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser  
 325 330 335  
 Leu Lys Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala  
 340 345 350  
 Val Val Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val  
 355 360 365  
 Ala Tyr Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val  
 370 375 380  
 Gly Leu Ser Gly Ala Pro Ala Asp Ala Cys Ser Tyr Ala Gln Lys Ala  
 385 390 395 400  
 Val Gly Tyr Ile Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu  
 405 410 415  
 Phe Ala Glu His Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys  
 420 425 430  
 Gln Lys

<210> 3  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1077)

<400> 3  
 atg ccg ctg gag ctg gag ctg tgt ccc ggg cgc tgg gtg ggc ggg caa 48  
 Met Pro Leu Glu Leu Glu Leu Cys Pro Gly Arg Trp Val Gly Gly Gln  
 1 5 10 15  
 cac ccg tgc ttc atc att gcc gag atc ggc cag aac cac cag ggc gac 96  
 His Pro Cys Phe Ile Ile Ala Glu Ile Gly Gln Asn His Gln Gly Asp  
 20 25 30  
 ctg gac gta gcc aag cgc atg atc cgc atg gcc aag gag tgt ggg gct 144  
 Leu Asp Val Ala Lys Arg Met Ile Arg Met Ala Lys Glu Cys Gly Ala  
 35 40 45  
 gat tgt gcc aag ttc cag aag agt gag cta gaa ttc aag ttt aat cgg 192  
 Asp Cys Ala Lys Phe Gln Lys Ser Glu Leu Glu Phe Lys Phe Asn Arg  
 50 55 60  
 aaa gcc ttg gag agg cca tac acc tcg aag cat tcc tgg ggg aag acg 240  
 Lys Ala Leu Glu Arg Pro Tyr Thr Ser Lys His Ser Trp Gly Lys Thr  
 65 70 75 80

tac ggg gag cac aaa cga cat ctg gag ttc agc cat gac cag tac agg	288
Tyr Gly Glu His Lys Arg His Leu Glu Phe Ser His Asp Gln Tyr Arg	
85 90 95	
gag ctg cag agg tac gcc gag gag gtt ggg atc ttc ttc act gcc tct	336
Glu Leu Gln Arg Tyr Ala Glu Glu Val Gly Ile Phe Phe Thr Ala Ser	
100 105 110	
ggc atg gat gag atg gca gtt gaa ttc ctg cat gaa ctg aat gtt cca	384
Gly Met Asp Glu Met Ala Val Glu Phe Leu His Glu Leu Asn Val Pro	
115 120 125	
ttt ttc aaa gtt gga tct gga gac act aat aat ttt cct tat ctg gaa	432
Phe Phe Lys Val Gly Ser Gly Asp Thr Asn Asn Phe Pro Tyr Leu Glu	
130 135 140	
aag aca gcc aaa aaa ggt cgc cca atg gtg atc tcc agt ggg atg cag	480
Lys Thr Ala Lys Lys Gly Arg Pro Met Val Ile Ser Ser Gly Met Gln	
145 150 155 160	
tca atg gac acc atg aag caa gtt tat cag atc gtg aag ccc ctc aac	528
Ser Met Asp Thr Met Lys Gln Val Tyr Gln Ile Val Lys Pro Leu Asn	
165 170 175	
ccc aac ttc tgc ttc ttg cag tgt acc agc gca tac ccg ctc cag cct	576
Pro Asn Phe Cys Phe Leu Gln Cys Thr Ser Ala Tyr Pro Leu Gln Pro	
180 185 190	
gag gac gtc aac ctg cgg gtc atc tcg gaa tat cag aag ctc ttt cct	624
Glu Asp Val Asn Leu Arg Val Ile Ser Glu Tyr Gln Lys Leu Phe Pro	
195 200 205	
gac att ccc ata ggg tat tct ggg cat gaa aca ggc ata gcg ata tct	672
Asp Ile Pro Ile Gly Tyr Ser Gly His Glu Thr Gly Ile Ala Ile Ser	
210 215 220	
gtg gcc gca gtg gct ctg ggg gcc aag gtg ttg gaa cgt cac ata act	720
Val Ala Ala Val Ala Leu Gly Ala Lys Val Leu Glu Arg His Ile Thr	
225 230 235 240	
ttg gac aag acc tgg aag ggg agt gac cac tcg gcc tcg ctg gag cct	768
Leu Asp Lys Thr Trp Lys Gly Ser Asp His Ser Ala Ser Leu Glu Pro	
245 250 255	
gga gaa ctg gcc gag ctg gtg cgg tca gtg cgt ctt gtg gag cgt gcc	816
Gly Glu Leu Ala Glu Leu Val Arg Ser Val Arg Leu Val Glu Arg Ala	
260 265 270	
ctg ggc tcc cca acc aag cag ctg ctg ccc tgt gag atg gcc tgc aat	864
Leu Gly Ser Pro Thr Lys Gln Leu Leu Pro Cys Glu Met Ala Cys Asn	
275 280 285	
gag aag ctg ggc aag tct gtg gtg gcc aaa gtg aaa att ccg gaa ggc	912
Glu Lys Leu Gly Lys Ser Val Val Ala Lys Val Lys Ile Pro Glu Gly	
290 295 300	
acc att cta aca atg gac atg ctc acc gtg aag gtg ggt gag ccc aaa	960
Thr Ile Leu Thr Met Asp Met Leu Thr Val Lys Val Gly Glu Pro Lys	
305 310 315 320	

gcc tat cct cct gaa gac atc ttt aat cta gtg ggc aag aag gtc ctg 1008  
 Ala Tyr Pro Pro Glu Asp Ile Phe Asn Leu Val Gly Lys Lys Val Leu  
 325 330 335

gtc act gtt gaa gag gat gac acc atc atg gaa gaa ttg gta gat aat 1056  
 Val Thr Val Glu Glu Asp Asp Thr Ile Met Glu Glu Leu Val Asp Asn  
 340 345 350

cat ggc aaa aaa atc aag tct taa 1080  
 His Gly Lys Lys Ile Lys Ser  
 355

<210> 4  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Met Pro Leu Glu Leu Glu Leu Cys Pro Gly Arg Trp Val Gly Gly Gln  
 1 5 10 15  
 His Pro Cys Phe Ile Ile Ala Glu Ile Gly Gln Asn His Gln Gly Asp  
 20 25 30  
 Leu Asp Val Ala Lys Arg Met Ile Arg Met Ala Lys Glu Cys Gly Ala  
 35 40 45  
 Asp Cys Ala Lys Phe Gln Lys Ser Glu Leu Glu Phe Lys Phe Asn Arg  
 50 55 60  
 Lys Ala Leu Glu Arg Pro Tyr Thr Ser Lys His Ser Trp Gly Lys Thr  
 65 70 75 80  
 Tyr Gly Glu His Lys Arg His Leu Glu Phe Ser His Asp Gln Tyr Arg  
 85 90 95  
 Glu Leu Gln Arg Tyr Ala Glu Glu Val Gly Ile Phe Phe Thr Ala Ser  
 100 105 110  
 Gly Met Asp Glu Met Ala Val Glu Phe Leu His Glu Leu Asn Val Pro  
 115 120 125  
 Phe Phe Lys Val Gly Ser Gly Asp Thr Asn Asn Phe Pro Tyr Leu Glu  
 130 135 140  
 Lys Thr Ala Lys Lys Gly Arg Pro Met Val Ile Ser Ser Gly Met Gln  
 145 150 155 160  
 Ser Met Asp Thr Met Lys Gln Val Tyr Gln Ile Val Lys Pro Leu Asn  
 165 170 175  
 Pro Asn Phe Cys Phe Leu Gln Cys Thr Ser Ala Tyr Pro Leu Gln Pro  
 180 185 190  
 Glu Asp Val Asn Leu Arg Val Ile Ser Glu Tyr Gln Lys Leu Phe Pro  
 195 200 205  
 Asp Ile Pro Ile Gly Tyr Ser Gly His Glu Thr Gly Ile Ala Ile Ser  
 210 215 220

Val Ala Ala Val Ala Leu Gly Ala Lys Val Leu Glu Arg His Ile Thr  
 225 230 235 240  
 Leu Asp Lys Thr Trp Lys Gly Ser Asp His Ser Ala Ser Leu Glu Pro  
 245 250 255  
 Gly Glu Leu Ala Glu Leu Val Arg Ser Val Arg Leu Val Glu Arg Ala  
 260 265 270  
 Leu Gly Ser Pro Thr Lys Gln Leu Leu Pro Cys Glu Met Ala Cys Asn  
 275 280 285  
 Glu Lys Leu Gly Lys Ser Val Val Ala Lys Val Lys Ile Pro Glu Gly  
 290 295 300  
 Thr Ile Leu Thr Met Asp Met Leu Thr Val Lys Val Gly Glu Pro Lys  
 305 310 315 320  
 Ala Tyr Pro Pro Glu Asp Ile Phe Asn Leu Val Gly Lys Lys Val Leu  
 325 330 335  
 Val Thr Val Glu Glu Asp Asp Thr Ile Met Glu Glu Leu Val Asp Asn  
 340 345 350  
 His Gly Lys Lys Ile Lys Ser  
 355

<210> 5  
 <211> 1429  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(690)

<400> 5  
 atg gcc ttc cca aag aag aaa ctt cag ggt ctt gtg gct gca acc atc 48  
 Met Ala Phe Pro Lys Lys Lys Leu Gln Gly Leu Val Ala Ala Thr Ile  
 1 5 10 15  
 acg cca atg act gag aat gga gaa atc aac ttt tca gta att ggt cag 96  
 Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln  
 20 25 30  
 tat gtg gat tat ctt gtg aaa gaa cag gga gtg aag aac att ttt gtg 144  
 Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val  
 35 40 45  
 aat ggc aca aca gga gaa ggc ctg tcc ctg agc gtc tca gag cgt cgc 192  
 Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg  
 50 55 60  
 cag gtt gca gag gag tgg gtg aca aaa ggg aag gac aag ctg gat cag 240  
 Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln  
 65 70 75 80  
 gtg ata att cac gta gga gca ctg agc ttg aag gag tca cag gaa ctg 288  
 Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu



85										90					95																
gcc	caa	cat	gca	gca	gaa	ata	gga	gct	gat	ggc	atc	gct	gtc	att	gca	336															
Ala	Gln	His	Ala	Ala	Glu	Ile	Gly	Ala	Asp	Gly	Ile	Ala	Val	Ile	Ala																
			100					105					110																		
ccg	ttc	ttc	ctc	aag	cca	tgg	acc	aaa	gat	atc	ctg	att	aat	ttc	cta	384															
Pro	Phe		Leu	Lys	Pro	Trp	Thr	Lys	Asp	Ile	Leu	Ile	Asn	Phe	Leu																
		115					120					125																			
aag	gaa	gtg	gct	gct	gcc	gcc	cct	gcc	ctg	cca	ttt	tat	tac	tat	cac	432															
Lys	Glu	Val	Ala	Ala	Ala	Ala	Pro	Ala	Leu	Pro	Phe	Tyr	Tyr	Tyr	His																
	130					135					140																				
att	cct	gcc	ttg	aca	ggg	gta	aag	att	cgt	gct	gag	gag	ttg	ttg	gat	480															
Ile	Pro	Ala	Leu	Thr	Gly	Val	Lys	Ile	Arg	Ala	Glu	Glu	Leu	Leu	Asp																
145					150				155						160																
ggg	att	ctg	gat	aag	atc	ccc	acc	ttc	caa	ggg	ctg	aaa	ttc	agt	gat	528															
Gly	Ile	Leu	Asp	Lys	Ile	Pro	Thr	Phe	Gln	Gly	Leu	Lys	Phe	Ser	Asp																
				165					170					175																	
aca	gat	ctc	tta	gac	ttc	ggg	caa	tgt	ggt	gat	cag	aat	cgc	cag	caa	576															
Thr	Asp	Leu	Leu	Asp	Phe	Gly	Gln	Cys	Val	Asp	Gln	Asn	Arg	Gln	Gln																
		180					185						190																		
cag	ttt	gct	ttc	ctt	ttt	ggg	gtg	gat	gag	caa	ctg	ttg	agt	gct	ctg	624															
Gln	Phe	Ala	Phe	Leu	Phe	Gly	Val	Asp	Glu	Gln	Leu	Leu	Ser	Ala	Leu																
	195					200						205																			
gtg	atg	gga	gca	act	gga	gca	gtg	ggc	agt	ttt	gta	tcc	aga	gat	tta	672															
Val	Met	Gly	Ala	Thr	Gly	Ala	Val	Gly	Ser	Phe	Val	Ser	Arg	Asp	Leu																
	210					215					220																				
tca	act	ttg	ttg	tca	aac	taggttttgg	agtgtcacag	accaaagcca								720															
Ser	Thr	Leu	Leu	Ser	Asn																										
225					230																										
tc	atg	act	ct	ggt	ct	ctg	ggg	att	cca	atg	g	ccc	ac	cccg	gct	tcc	act	g	cag	aa	gc	ct	780								
cc	agg	g	agt	t	act	gat	agt	g	ct	ga	ag	cta	a	act	ga	ag	ag	c	ct	g	g	att	t	c	ctt	ctt	t	ca	840		
ct	g	att	t	ta	aa	gg	at	g	ga	ag	ct	g	g	ta	g	ct	g	ta	g	ct	g	ta	g	ct	g	ta	g	ct	g	900	
tt	g	ca	ct	tt	g	ag	ca	ta	at	c	tac	ct	ta	aa	t	agt	gc	at	t	t	t	t	c	ag	gg	g	g	g	g	960	
ga	act	t	ga	at	aa	act	t	ct	ct	ag	ca	aa	t	ga	at	ct	ca	ca	at	aa	t	ga	at	ct	ca	ca	at	aa	t	ga	1020
tg	ag	cc	tt	aa	aa	gt	ct	tt	at	ttt	gt	ga	ag	gg	ca	aaa	a	act	ct	ag	tg	ca	ca	act	ct	ag	1080				
tc	att	ca	ttt	cac	ag	at	ttt	g	gg	aga	a	att	t	ct	gt	t	t	at	at	g	g	at	g	aa	t	g	ga	at	c	1140	
aa	g	ag	g	aaaa	tt	g	ta	att	g	ga	tt	aa	ct	ct	g	ag	gc	ta	ct	ct	ca	t	at	ct	cg	gt	c	1200			
t	ct	g	gt	tc	ct	aat	ct	at	ttt	t	aa	ag	tt	gt	c	ta	att	t	ta	aa	aa	cc	act	ta	at	at	gt	ct	tt	ca	1260
tt	ta	ata	aa	at	tt	ca	tt	tg	g	aat	ct	ag	ga	a	act	ct	g	ag	c	t	act	g	at	tt	ag	g	c	ag	g	c	1320
tt	ta	ata	cca	a	act	g	ta	aca	a	gt	ct	ca	act	gt	ata	ca	act	ca	aa	a	ta	ca	c	ag	ct	ca	tt	t	1380		
gg	ct	g	ct	ca	g	t	ct	ca	g	at	g	g	at	g	c	t	tt	g	aa	tt	c	at	tt	cg	at	g	1429				

<210> 6  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Ala Phe Pro Lys Lys Lys Leu Gln Gly Leu Val Ala Ala Thr Ile  
   1                  5                  10                  15  
 Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln  
                   20                  25                  30  
 Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val  
                   35                  40                  45  
 Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg  
   50                  55                  60  
 Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln  
   65                  70                  75                  80  
 Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu  
                   85                  90                  95  
 Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala  
                   100                  105                  110  
 Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu  
                   115                  120                  125  
 Lys Glu Val Ala Ala Ala Ala Pro Ala Leu Pro Phe Tyr Tyr Tyr His  
   130                  135                  140  
 Ile Pro Ala Leu Thr Gly Val Lys Ile Arg Ala Glu Glu Leu Leu Asp  
  145                  150                  155                  160  
 Gly Ile Leu Asp Lys Ile Pro Thr Phe Gln Gly Leu Lys Phe Ser Asp  
                   165                  170                  175  
 Thr Asp Leu Leu Asp Phe Gly Gln Cys Val Asp Gln Asn Arg Gln Gln  
                   180                  185                  190  
 Gln Phe Ala Phe Leu Phe Gly Val Asp Glu Gln Leu Leu Ser Ala Leu  
                   195                  200                  205  
 Val Met Gly Ala Thr Gly Ala Val Gly Ser Phe Val Ser Arg Asp Leu  
   210                  215                  220  
 Ser Thr Leu Leu Ser Asn  
 225                  230